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<120> Regulation of Angiogenesis With Zinc  
Finger Proteins

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<151> 2000-12-07

<150> US 09/736,083  
<151> 2000-12-12

<150> US 09/846,033  
<151> 2001-04-30

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&lt;223&gt; finger

&lt;400&gt; 174

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&lt;210&gt; 175

&lt;211&gt; 7

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&lt;220&gt;

&lt;223&gt; finger

&lt;400&gt; 175

Arg Ser Asp Asn Leu Thr Gln  
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&lt;211&gt; 7

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&lt;223&gt; finger

&lt;400&gt; 176

Asp Arg Ser Ser Leu Thr Arg  
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&lt;223&gt; finger

&lt;400&gt; 177

Arg Ser Asp His Leu Ser Arg  
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&lt;211&gt; 7

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&lt;220&gt;

&lt;223&gt; finger

&lt;400&gt; 178

Gln Ser Gly Ser Leu Thr Arg  
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&lt;210&gt; 179

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<223> VEGF-C reverse primer

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tgaacagggtc tcttcatcca gc

22

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<221> modified\_base

<222> (26)...(26)

<223> n = a modified by tetramethylrhodamine (TAMRA)

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26

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19

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class of zinc finger proteins (ZFP)

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<222> (2)...(5)

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be present or absent

<221> MOD\_RES

<222> (7)...(18)

<223> Xaa = any amino acid

<221> MOD\_RES

<222> (20)...(24)

<223> Xaa = any amino acid, Xaa in positions 23 and 24  
may be present or absent

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 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His  
 20 25

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9

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<400> 210  
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9

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<400> 211  
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<210> 212  
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<400> 212  
 Gly Gly Gly Gly Ser  
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Gly Gly Arg Arg Gly Gly Gly Ser  
1 5

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Leu Arg Gln Arg Asp Gly Glu Arg Pro  
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Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro  
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factor Zif268

<400> 217

Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp  
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Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro  
20 25 30

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## factor Zif268

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Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu  
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 Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro  
                     20                      25

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&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; F3 DNA binding domain of mouse transcription factor Zif268

&lt;400&gt; 219

Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg  
 1                      5                      10                      15  
 Lys Arg His Thr Lys Ile His Leu Arg Gln Lys  
                     20                      25

&lt;210&gt; 220

&lt;211&gt; 9

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mouse transcription factor Zif268 target

&lt;400&gt; 220

gcgtgggcg

9

&lt;210&gt; 221

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Sp-1 transcription factor

&lt;400&gt; 221

Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys Gly Lys  
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                     20                      25                      30  
 Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe  
                     35                      40                      45  
 Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr Gly Glu  
                     50                      55                      60  
 Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp  
 65                      70                      75                      80  
 His Leu Ser Lys His Ile Lys Thr His Gln Asn Lys Lys Gly  
                     85                      90

&lt;210&gt; 222

&lt;211&gt; 9

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Sp-1 optimal target consensus sequence

&lt;400&gt; 222

ggggcgggg

9

&lt;210&gt; 223

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Sp-i consensus sequence with leader sequence

&lt;400&gt; 223

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Lys | Leu | Arg | Asn | Gly | Ser | Gly | Asp | Pro | Gly | Lys | Lys | Lys | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| His | Ala | Cys | Pro | Glu | Cys | Gly | Lys | Ser | Phe | Ser | Lys | Ser | Ser | His | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ala | His | Gln | Arg | Thr | His | Thr | Gly | Glu | Arg | Pro | Tyr | Lys | Cys | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Cys | Gly | Lys | Ser | Phe | Ser | Arg | Ser | Asp | Glu | Leu | Gln | Arg | His | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Thr | His | Thr | Gly | Glu | Lys | Pro | Tyr | Lys | Cys | Pro | Glu | Cys | Gly | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Phe | Ser | Arg | Ser | Asp | His | Leu | Ser | Lys | His | Gln | Arg | Thr | His | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Lys | Lys | Gly |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 224

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; N-terminal nuclear localization signal from SV40 large T antigen

&lt;400&gt; 224

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Lys | Lys | Arg | Lys | Val |
| 1   |     |     |     | 5   |     |     |

&lt;210&gt; 225

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; FLAG peptide

&lt;400&gt; 225

|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Lys | Asp | Asp | Asp | Asp | Lys |
| 1   |     |     |     | 5   |     |     |     |

&lt;210&gt; 226

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> VEGF-A forward primer

<400> 226  
gtgcattgga gccttgccctt g 21

<210> 227  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> VEGF-A reverse primer

<400> 227  
actcgatctc atcagggtac tc 22

<210> 228  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> VEGF-A Taqman probe

<221> modified\_base  
<222> (1)...(1)  
<223> n = c modified by aminofluorescein (FAM)

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<221> modified\_base  
<222> (25)...(25)  
<223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 228  
nagtagctgc gctgatagac atccn 25

<210> 229  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GAPDH forward primer

<400> 229  
ccatgttcgt catgggtgtg a 21

<210> 230  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GAPDH reverse primer

<400> 230  
catggactgt ggtcatgagt 20

<210> 231  
<211> 24  
<212> DNA  
<213> Artificial Sequence

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<220>
<223> GAPDH Taqman probe

<221> modified_base
<222> (1)...(1)
<223> n = t modified by aminofluorescein (FAM)

<221> modified_base
<222> (24)...(24)
<223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 231
ncctgcacca ccaactgctt agcn                                     24

<210> 232
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> VP16-FLAG forward primer

<400> 232
catgacgatt tcgatctgga                                         20

<210> 233
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> VP16-FLAG reverse primer

<400> 233
ctacttgatca tcgtcgtcct tg                                     22

<210> 234
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> VP16-FLAG Taqman probe

<221> modified_base
<222> (1)...(1)
<223> n = a modified by aminofluorescein (FAM)

<221> modified_base
<222> (26)...(26)
<223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 234
ntcggtaaac atctgctcaa actcgn                                     26

<210> 235
<211> 28
<212> DNA
<213> Artificial Sequence

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<220>  
 <223> RT-PCR primer  
  
 <400> 235  
 atgaactttc tgctgtcttg ggtgcatt 28  
  
 <210> 236  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> RT-PCR primer  
  
 <400> 236  
 tcaccgcctc ggcttgtcac at 22  
  
 <210> 237  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> murine VEGF target  
  
 <400> 237  
 tgagcggcgg cagcggag 18  


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 <210> 238  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> recognition helix  
  
 <400> 238  
 Arg Ser Asp Glu Leu Ser Arg  
 1 5  
  
 <210> 239  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> recognition helix  
  
 <400> 239  
 Gln Ser Gly His Leu Thr Lys  
 1 5  
  
 <210> 240  
 <211> 10  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> target  
  
 <400> 240



gctgggggcg

10

<210> 241  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 241  
 cccagatctg gtgatggcaa gaagaagcag caccatctgc cacatccag

49

<210> 242  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 242  
 cccaagctta ggatccaccc ttcttgttct ggtgggt

37

<210> 243  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VZ+57

<400> 243  
 His Gln Asn Lys Lys Gly Gly Ser Gly Asp Gly Lys Lys Lys Gln His  
 1 5 10 15  
 Ile Cys

<210> 244  
 <211> 9  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> target

<400> 244  
 gaggcttg

9

<210> 245  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> finger

<400> 245  
 Thr Ser Gly His Leu Thr Arg  
 1 5

<210> 246  
 <211> 7  
 <212> PRT  
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<220>  
 <223> finger

<400> 246  
 Thr Ser Gly His Leu Ile Arg  
 1 5

<210> 247  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> finger

<400> 247  
 Thr Ser Gly His Leu Ser Arg  
 1 5

<210> 248  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> finger

<400> 248  
 Thr Ser Gly His Leu Ala Arg  
 1 5

<210> 249  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> finger

<400> 249  
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 1 5

<210> 250  
 <211> 7  
 <212> PRT  
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<220>  
 <223> finger

<400> 250  
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 1 5

<210> 251  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> finger

<400> 251  
Thr Thr Gly His Leu Val Arg  
1 5

<210> 252  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> finger

<400> 252  
Thr Lys Asp His Leu Val Arg  
1 5

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